Amendments to the Specification:

Please amend the paragraph beginning on page 10, line 17, as follows:

Methods of determining percent identity are known in the art. "Percent (%) sequence identity" with respect to a specified subject sequence, or a specified portion thereof, may be defined as the percentage of nucleotides or amino acids in the candidate derivative sequence identical with the nucleotides or amino acids in the subject sequence (or specified portion thereof), after aligning the sequences and introducing gaps, if necessary to achieve the maximum percent sequence identity, as generated by the program WU-BLAST-2.0a19 (Altschul et al., J. Mol. Biol. 215:403-410 (1997); ~~http://~~blast.wustl.edu/blast/README.htm- l) with search parameters set to default values. The HSP S and HSP S2 parameters are dynamic values and are established by the program itself depending upon the composition of the particular sequence and composition of the particular database against which the sequence of interest is being searched. A "% identity value" is determined by the number of matching identical nucleotides or amino acids divided by the sequence length for which the percent identity is being reported.

Please amend the paragraph beginning on page 14, line 8, as follows:

SEQ ID NOs: 1 and 2 depict the amino acid sequences of the full-length wild-type human and mouse PTN, respectively. A "functionally active" PTN fragment or derivative exhibits one or more functional activities associated with a full-length, wild-type PTN protein, such as antigenic or immunogenic activity, ability to bind natural cellular substrates, etc. The functional activity of PTN proteins, derivatives and fragments can be assayed by various methods known to one skilled in the art (Current Protocols in Protein Science, Coligan et al., eds., John Wiley & Sons, Inc., Somerset, N.J. (1998)). For purposes herein, functionally active fragments also include those fragments that comprise one or more structural domains of a PTN polypeptide, such as a binding domain. Protein domains can be identified using the PFAM program (Bateman A., et al., Nucleic Acids Res. 27: 260-2 (1999); ~~http://~~pfam.wustl.edu).

Please amend the paragraph beginning on page 24, line 1, as follows:

The method of producing an isolated antibody against a protein comprises 1) selecting a host animal; 2) immunizing said host animal with a fusion protein comprising said protein connected

with a T-cell epitope. A "T-cell epitope" is defined as a peptide sequence recognized by the T-cell receptor of T helper cells in the context of MHC molecules. Upon binding to one or more of these T-cell epitopes, the T helper cells can be activated and recruit T-cells. The present methods can use any T-cell epitopes known in the art, for example, OVA and cytochrome ~~cytochorme~~ C peptide. Additional examples are the T-cell epitopes disclosed in U.S. Pat. Nos: 6,143,935, 5,785,973, and 6,419,931. The T-cell epitopes can be connected to the C-terminus or N-terminus of said protein, or inserted in the suitable positions between N-terminus and C-terminus of said protein as long as the connection will not detrimentally affect either the antigenic utility of said protein or the binding utility of the T-cell epitopes with T helper cells. In one example, where the antibodies against PTN are intended to be made, the N-terminus of OVA peptide can be inserted after position 124 of SEQ ID NO: 1. Standard molecular cloning techniques are used to link a DNA molecule encoding a T-cell epitope to a DNA molecule encoding said antigenic protein, so that a DNA molecule encoding the fusion protein is created. Expression vectors comprising the DNA molecules encoding the fusion protein are then transfected to any expression systems to produce the desired fusion protein. The expression systems include both prokaryotic and eukaryotic expression systems, such as bacteria, yeast, insect cells, plant cells, and mammalian cells.

Please amend the paragraph beginning on page 26, line 5, as follows:

The methods of the present invention offer at least two advantages as compared to the conventional methods of making polyclonal and monoclonal antibodies. First, the present methods can produce antibodies, especially neutralizing antibodies against proteins that are highly homologous among the mammalian species. The highly homologous proteins usually play key roles in important physiological pathways in mammals including human. Unfortunately, it is very difficult to elicit the immune response of these proteins in a rodent. The present methods have opened a new avenue ~~revenue~~ for the immunotherapy targeted to these proteins. Second, it is desirable in the clinical studies to produce an antibody that binds to a target antigen of human as well as that of other mammalian species (e.g., mouse, rat, rabbit, etc.), which will be used in a pre-clinical disease model. Such an antibody can thus be used for both pre-clinical studies with a model animal and for clinical studies with humans, saving a great deal of time and resources in the drug

development process. The antibodies produced by the present methods will preferably have such characteristics.